

10/525567

DT01 Rec'd PCT/PTO 25 FEB 2005

SEQUENCE LISTING

<110> Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo

<120> Anti-allergic agent

<130> W0961

<160> 12

<210> 1

<211> 10

<212> PRT

<213> Apis mellifera

<400> 1

Ala Ala Val Asn His Gln Arg Lys Ser Ala

1 5 10

<210> 2

<211> 25

<212> PRT

<213> Apis mellifera

<400> 2

Asn Ile Leu Arg Gly Glu Ser Leu Asn Lys Ser Leu Pro Ile Leu His

1 5 10 15

Glu Trp Lys Phe Phe Asp Tyr Asp Phe

20 25

<210> 3

<211> 524

<212> PRT

<213> Apis mellifera

<400> 3

Ala Ala Val Asn His Gln Arg Lys Ser Ala Asn Asn Leu Ala His Ser

1 5 10 15

Met	Lys	Val	Ile	Tyr	Glu	Trp	Lys	His	Ile	Asp	Phe	Asp	Phe	Gly	Ser	20	25	30	
Asp	Glu	Arg	Arg	Asp	Ala	Ala	Ile	Lys	Ser	Gly	Glu	Phe	Asp	His	Thr	35	40	45	
Lys	Asn	Tyr	Pro	Phe	Asp	Val	Asp	Arg	Trp	Arg	Asp	Lys	Thr	Phe	Val	50	55	60	
Thr	Ile	Glu	Arg	Asn	Asn	Gly	Val	Pro	Ser	Ser	Leu	Asn	Val	Val	Thr	65	70	75	80
Asn	Lys	Lys	Gly	Lys	Gly	Gly	Pro	Leu	Leu	Arg	Pro	Tyr	Pro	Asp	Trp	85	90	95	
Ser	Phe	Ala	Lys	Tyr	Glu	Asp	Cys	Ser	Gly	Ile	Val	Ser	Ala	Phe	Lys	100	105	110	
Ile	Ala	Val	Asp	Lys	Phe	Asp	Arg	Leu	Trp	Val	Leu	Asp	Ser	Gly	Leu	115	120	125	
Val	Asn	Asn	Asn	Gln	Pro	Met	Cys	Ser	Pro	Lys	Leu	Leu	Thr	Phe	Asp	130	135	140	
Leu	Lys	Thr	Ser	Lys	Leu	Val	Lys	Gln	Val	Glu	Ile	Pro	His	Asn	Ile	145	150	155	160
Ala	Val	Asn	Ala	Thr	Thr	Gly	Met	Gly	Glu	Leu	Val	Ser	Leu	Ala	Val	165	170	175	
Gln	Ala	Ile	Asp	Arg	Thr	Asn	Thr	Met	Val	Tyr	Ile	Ala	Asp	Glu	Lys	180	185	190	
Gly	Glu	Gly	Leu	Ile	Met	Tyr	Gln	Asn	Ser	Asp	Asp	Ser	Phe	His	Arg	195	200	205	

Leu Thr Ser Asn Thr Phe Asp Tyr Asp Pro Arg Tyr Thr Lys Leu Thr			
210	215	220	
Val Ala Gly Glu Ser Phe Thr Val Lys Asn Gly Ile Cys Gly Ile Ala			
225	230	235	240
Leu Ser Pro Val Thr Asn Asn Leu Tyr Tyr Ser Pro Leu Ser Ser His			
	245	250	255
Gly Leu Tyr Tyr Val Asp Thr Glu Gln Phe Arg Asn Pro Gln Tyr Glu			
	260	265	270
Glu Asn Asn Val Gln Tyr Glu Gly Ser Gln Asp Ile Leu Asn Thr Gln			
	275	280	285
Ser Phe Gly Lys Val Val Ser Lys Asn Gly Val Leu Phe Leu Gly Leu			
	290	295	300
Val Gly Asn Ser Gly Ile Ala Cys Val Asn Glu His Gln Val Leu Gln			
305	310	315	320
Arg Glu Ser Phe Asp Val Val Ala Gln Asn Glu Glu Thr Leu Gln Met			
	325	330	335
Ile Val Ser Met Lys Ile Met Glu Asn Leu Pro Gln Ser Gly Arg Ile			
	340	345	350
Asn Asp Pro Glu Gly Asn Glu Tyr Met Leu Ala Leu Ser Asn Arg Met			
	355	360	365
Gln Lys Ile Ile Asn Asn Asp Phe Asn Phe Asn Asp Val Asn Phe Arg			
	370	375	380
Ile Leu Gly Ala Asn Val Asp Asp Leu Met Arg Asn Thr Arg Cys Gly			
385	390	395	400

Arg Tyr His Asn Gln Asn Ala Gly Asn Gln Asn Ala Asp Asn Gln Asn
405 410 415

Ala Asp Asn Gln Asn Ala Asn Asn Gln Asn Ala Asp Asn Gln Asn Ala
420 425 430

Asn Lys Gln Asn Gly Asn Arg Gln Asn Asp Asn Arg Gln Asn Asp Asn
435 440 445

Lys Gln Asn Gly Asn Arg Gln Asn Asp Asn Lys Gln Asn Gly Asn Arg
450 455 460

Gln Asn Asp Asn Lys Gln Asn Gly Asn Arg Gln Asn Gly Asn Lys Gln
465 470 475 480

Asn Asp Asn Lys Gln Asn Gly Asn Arg Gln Asn Asp Asn Lys Arg Asn
485 490 495

Gly Asn Arg Gln Asn Asp Asn Gln Asn Asn Gln Asn Asp Asn Asn Arg
500 505 510

Asn Asp Asn Gln Val His His Ser Ser Lys Leu His
515 520

<210> 4

<211> 413

<212> PRT

<213> Apis mellifera

<400> 4

Asn Ile Leu Arg Gly Glu Ser Leu Asn Lys Ser Leu Pro Ile Leu His
1 5 10 15

Glu Trp Lys Phe Phe Asp Tyr Asp Phe Gly Ser Asp Glu Arg Arg Gln
20 25 30

Asp Ala Ile Leu Ser Gly Glu Tyr Asp Tyr Lys Asn Asn Tyr Pro Ser
35 40 45

Asp Ile Asp Gln Trp His Asp Lys Ile Phe Val Thr Met Leu Arg Tyr
50 55 60

Asn Gly Val Pro Ser Ser Leu Asn Val Ile Ser Lys Lys Val Gly Asp
65 70 75 80

Gly Gly Pro Leu Leu Gln Pro Tyr Pro Asp Trp Ser Phe Ala Lys Tyr
85 90 95

Asp Asp Cys Ser Gly Ile Val Ser Ala Ser Lys Leu Ala Ile Asp Lys
100 105 110

Cys Asp Arg Leu Trp Val Leu Asp Ser Gly Leu Val Asn Asn Thr Gln
115 120 125

Pro Met Cys Ser Pro Lys Leu Leu Thr Phe Asp Leu Thr Thr Ser Gln
130 135 140

Leu Leu Lys Gln Val Glu Ile Pro His Asp Val Ala Val Asn Ala Thr
145 150 155 160

Thr Gly Lys Gly Arg Leu Ser Ser Leu Ala Val Gln Ser Leu Asp Cys
165 170 175

Asn Thr Asn Ser Asp Thr Met Val Tyr Ile Ala Asp Glu Lys Gly Glu
180 185 190

Gly Leu Ile Val Tyr His Asn Ser Asp Asp Ser Phe His Arg Leu Thr
195 200 205

Ser Asn Thr Phe Asp Tyr Asp Pro Lys Phe Thr Lys Met Thr Ile Asp
210 215 220

Gly Glu Ser Tyr Thr Ala Gln Asp Gly Ile Ser Gly Met Ala Leu Ser
 225 230 235 240

Pro Met Thr Asn Asn Leu Tyr Tyr Ser Pro Val Ala Ser Thr Ser Leu
 245 250 255

Tyr Tyr Val Asn Thr Glu Gln Phe Arg Thr Ser Asp Tyr Gln Gln Asn
 260 265 270

Asp Ile His Tyr Glu Gly Val Gln Asn Ile Leu Asp Thr Gln Ser Ser
 275 280 285

Ala Lys Val Val Ser Lys Ser Gly Val Leu Phe Phe Gly Leu Val Gly
 290 295 300

Asp Ser Ala Leu Gly Cys Trp Asn Glu His Arg Thr Leu Glu Arg His
 305 310 315 320

Asn Ile Arg Thr Val Ala Gln Ser Asp Glu Thr Leu Gln Met Ile Ala
 325 330 335

Ser Met Lys Ile Lys Glu Ala Xaa Pro His Val Pro Ile Phe Asp Arg
 340 345 350

Tyr Ile Asn Arg Glu Tyr Ile Leu Val Leu Ser Asn Lys Met Gln Lys
 355 360 365

Met Val Asn Asn Asp Phe Asn Phe Asp Asp Val Asn Phe Arg Ile Met
 370 375 380

Asn Ala Asn Val Asn Glu Leu Ile Leu Asn Thr Arg Cys Glu Asn Pro
 385 390 395 400

Asp Asn Asp Arg Thr Pro Phe Lys Ile Ser Ile His Leu
 405 410

<210> 5

<211> 1635

<212> DNA

<213> *Apis mellifera*

<220>

<221> CDS

<222> (1)..(1635)

<220>

<221> mat_peptide

<222> (61)..(1632)

<400> 5

atg aca aag tgg ttg ttg ctg gtg gtg tgc ctt ggt ata gct tgt caa 48
Met Thr Lys Trp Leu Leu Leu Val Val Cys Leu Gly Ile Ala Cys Gln
-20 -15 -10 -5

gat gta aca agc gca gct gtg aat cat caa aga aaa tct gca aat aat 96
Asp Val Thr Ser Ala Ala Val Asn His Gln Arg Lys Ser Ala Asn Asn
1 5 10

ttg gca cat tct atg aaa gtg atc tac gaa tgg aaa cac att gat ttt 144
Leu Ala His Ser Met Lys Val Ile Tyr Glu Trp Lys His Ile Asp Phe
15 20 25

gat ttc ggt agc gat gaa aga aga gat gct gcg att aaa tct ggc gaa 192
Asp Phe Gly Ser Asp Glu Arg Arg Asp Ala Ala Ile Lys Ser Gly Glu
30 35 40

ttt gat cac aca aaa aat tat cct ttc gat gtg gac aga tgg cgt gat 240
Phe Asp His Thr Lys Asn Tyr Pro Phe Asp Val Asp Arg Trp Arg Asp
45 50 55 60

aag aca ttt gtc acc ata gaa agg aac aat ggt gta cct tct tct ttg 288
Lys Thr Phe Val Thr Ile Glu Arg Asn Asn Gly Val Pro Ser Ser Leu
65 70 75

aac gtg gta act aat aaa aag ggc aaa ggt gga cct ctt cta cga cca 336

Asn Val Val Thr Asn Lys Lys Gly Lys Gly Gly Pro Leu Leu Arg Pro
80 85 90

tat cct gat tgg tcg ttt gcc aaa tac gaa gat tgc tct gga att gtg 384
Tyr Pro Asp Trp Ser Phe Ala Lys Tyr Glu Asp Cys Ser Gly Ile Val
95 100 105

agc gct ttc aaa att gcg gtc gac aaa ttt gac aga tta tgg gtt ctg 432
Ser Ala Phe Lys Ile Ala Val Asp Lys Phe Asp Arg Leu Trp Val Leu
110 115 120

gac tca ggt ctt gtc aat aat aat caa cct atg tgc tct cca aaa ttg 480
Asp Ser Gly Leu Val Asn Asn Asn Gln Pro Met Cys Ser Pro Lys Leu
125 130 135 140

tta acc ttt gat ctg aaa acc tca aaa ttg gtt aag caa gtc gag ata 528
Leu Thr Phe Asp Leu Lys Thr Ser Lys Leu Val Lys Gln Val Glu Ile
145 150 155

cca cat aat att gcc gta aac gcc acc aca gga atg gga gaa tta gtt 576
Pro His Asn Ile Ala Val Asn Ala Thr Thr Gly Met Gly Glu Leu Val
160 165 170

tca cta gct gtt caa gct ata gat cgt acg aat act atg gtg tac ata 624
Ser Leu Ala Val Gln Ala Ile Asp Arg Thr Asn Thr Met Val Tyr Ile
175 180 185

gca gac gaa aaa ggc gaa ggt tta atc atg tat caa aac tcc gac gat 672
Ala Asp Glu Lys Gly Glu Gly Leu Ile Met Tyr Gln Asn Ser Asp Asp
190 195 200

tcc ttc cat cga ttg act tcc aat act ttc gat tac gat ccc aga tat 720
Ser Phe His Arg Leu Thr Ser Asn Thr Phe Asp Tyr Asp Pro Arg Tyr
205 210 215 220

acc aaa ttg aca gtc gct gga gaa agt ttc aca gtg aaa aat gga att 768

Thr Lys Leu Thr Val Ala Gly Glu Ser Phe Thr Val Lys Asn Gly Ile
225 230 235

tgt gga att gca ctt agt ccc gtg acg aac aat ctt tat tac agc cct 816
Cys Gly Ile Ala Leu Ser Pro Val Thr Asn Asn Leu Tyr Tyr Ser Pro
240 245 250

ctc tct tct cac ggt ttg tat tat gtt gat acg gaa caa ttc agg aat 864
Leu Ser Ser His Gly Leu Tyr Tyr Val Asp Thr Glu Gln Phe Arg Asn
255 260 265

cca caa tat gaa gaa aat aac gtg caa tat gaa gga tct caa gat att 912
Pro Gln Tyr Glu Glu Asn Asn Val Gln Tyr Glu Gly Ser Gln Asp Ile
270 275 280

ttg aac act caa tca ttc ggt aaa gta gta tcg aaa aat ggc gtc ctt 960
Leu Asn Thr Gln Ser Phe Gly Lys Val Val Ser Lys Asn Gly Val Leu
285 290 295 300

ttc ttg gga ctc gtg ggt aat tca ggt att gcc tgc gtg aat gaa cat 1008
Phe Leu Gly Leu Val Gly Asn Ser Gly Ile Ala Cys Val Asn Glu His
305 310 315

caa gta ctt cag aga gaa agt ttt gat gtt gtc gct cag aat gaa gag 1056
Gln Val Leu Gln Arg Glu Ser Phe Asp Val Val Ala Gln Asn Glu Glu
320 325 330

aca ctt caa atg atc gtt agt atg aaa atc atg gaa aat ctt cca caa 1104
Thr Leu Gln Met Ile Val Ser Met Lys Ile Met Glu Asn Leu Pro Gln
335 340 345

tcc ggc aga att aat gat cct gaa ggc aat gaa tat atg ttg gct ttg 1152
Ser Gly Arg Ile Asn Asp Pro Glu Gly Asn Glu Tyr Met Leu Ala Leu
350 355 360

agt aac aga atg caa aaa ata ata aac aat gat ttt aat ttc aac gac 1200

Ser Asn Arg Met Gln Lys Ile Ile Asn Asn Asp Phe Asn Phe Asn Asp
 365 370 375 380

gta aat ttc cga att ttg ggt gcg aat gta gat gac tta atg aga aac 1248
 Val Asn Phe Arg Ile Leu Gly Ala Asn Val Asp Asp Leu Met Arg Asn
 385 390 395

act cgt tgc gga aga tat cac aat cag aat gct ggc aat cag aat gct 1296
 Thr Arg Cys Gly Arg Tyr His Asn Gln Asn Ala Gly Asn Gln Asn Ala
 400 405 410

gac aat cag aat gct gac aat cag aat gct aac aat cag aat gct gat 1344
 Asp Asn Gln Asn Ala Asp Asn Gln Asn Ala Asn Asn Gln Asn Ala Asp
 415 420 425

aat cag aat gct aac aaa caa aat ggt aat aga caa aat gat aac aga 1392
 Asn Gln Asn Ala Asn Lys Gln Asn Gly Asn Arg Gln Asn Asp Asn Arg
 430 435 440

cag aat gat aac aag caa aat ggt aac aga cag aat gat aac aag caa 1440
 Gln Asn Asp Asn Lys Gln Asn Gly Asn Arg Gln Asn Asp Asn Lys Gln
 445 450 455 460

aat ggt aac aga cag aat gat aac aag caa aat ggt aac aga caa aat 1488
 Asn Gly Asn Arg Gln Asn Asp Asn Lys Gln Asn Gly Asn Arg Gln Asn
 465 470 475

ggt aac aaa cag aat gat aac aag caa aat ggt aac aga cag aat gat 1536
 Gly Asn Lys Gln Asn Asp Asn Lys Gln Asn Gly Asn Arg Gln Asn Asp
 480 485 490

aac aag agg aat ggt aac agg caa aat gat aat caa aat aat cag aat 1584
 Asn Lys Arg Asn Gly Asn Arg Gln Asn Asp Asn Gln Asn Asn Gln Asn
 495 500 505

gat aat aat cga aat gat aat caa gtt cat cat tct tca aaa tta cat 1632

Asp Asn Asn Arg Asn Asp Asn Gln Val His His Ser Ser Lys Leu His
 510 515 520

taa 1635

<210> 6

<211> 1245

<212> DNA

<213> *Apis mellifera*

<220>

<221> CDS

<222> (1)..(1245)

<220>

<221> mat_peptide

<222> (4)..(1242)

<400> 6

atg aac att ctt cga gga gag tct tta aac aaa tca tta ccc atc ctt 48
 Met Asn Ile Leu Arg Gly Glu Ser Leu Asn Lys Ser Leu Pro Ile Leu
 -1 1 5 10 15

cac gaa tgg aaa ttc ttt gat tat gat ttc ggt agc gat gaa aga aga 96
 His Glu Trp Lys Phe Phe Asp Tyr Asp Phe Gly Ser Asp Glu Arg Arg
 20 25 30

caa gat gca att cta tct ggc gaa tac gac tac aag aat aat tat cca 144
 Gln Asp Ala Ile Leu Ser Gly Glu Tyr Asp Tyr Lys Asn Asn Tyr Pro
 35 40 45

tcc gac att gac caa tgg cat gat aag att ttt gtc acc atg ctg aga 192
 Ser Asp Ile Asp Gln Trp His Asp Lys Ile Phe Val Thr Met Leu Arg
 50 55 60

tac aat ggc gta cct tcc tct ttg aac gtg ata tct aaa aag gtc ggt 240
 Tyr Asn Gly Val Pro Ser Ser Leu Asn Val Ile Ser Lys Lys Val Gly

65	70	75	
gat ggt ggt cct ctt cta caa cct tat ccc gat tgg tcg ttt gct aaa 288			
Asp Gly Gly Pro Leu Leu Gln Pro Tyr Pro Asp Trp Ser Phe Ala Lys			
80	85	90	95
tat gac gat tgc tct gga atc gtg agc gcc tca aaa ctt gcg atc gac 336			
Tyr Asp Asp Cys Ser Gly Ile Val Ser Ala Ser Lys Leu Ala Ile Asp			
	100	105	110
aaa tgc gac aga ttg tgg gtt ctg gac tca ggt ctt gtc aat aat act 384			
Lys Cys Asp Arg Leu Trp Val Leu Asp Ser Gly Leu Val Asn Asn Thr			
	115	120	125
caa ccc atg tgt tct cca aaa ctg ctc acc ttt gat ctg act acc tcg 432			
Gln Pro Met Cys Ser Pro Lys Leu Leu Thr Phe Asp Leu Thr Thr Ser			
	130	135	140
caa ttg ctc aag caa gtt gaa ata cca cat gat gtt gcc gta aat gcc 480			
Gln Leu Leu Lys Gln Val Glu Ile Pro His Asp Val Ala Val Asn Ala			
	145	150	155
act aca gga aag gga aga tta tca tct cta gct gtt caa tct tta gat 528			
Thr Thr Gly Lys Gly Arg Leu Ser Ser Leu Ala Val Gln Ser Leu Asp			
160	165	170	175
tgc aat aca aat agc gat act atg gtg tac ata gca gac gag aaa ggt 576			
Cys Asn Thr Asn Ser Asp Thr Met Val Tyr Ile Ala Asp Glu Lys Gly			
	180	185	190
gaa ggt tta atc gtg tat cat aat tct gat gat tcc ttc cat cga ttg 624			
Glu Gly Leu Ile Val Tyr His Asn Ser Asp Asp Ser Phe His Arg Leu			
195	200	205	
act tcc aac act ttc gat tac gat cct aaa ttt acc aaa atg acg atc 672			
Thr Ser Asn Thr Phe Asp Tyr Asp Pro Lys Phe Thr Lys Met Thr Ile			

210	215	220	
gat gga gaa agt tac aca gcc caa gat gga att tct gga atg gct ctt 720			
Asp Gly Glu Ser Tyr Thr Ala Gln Asp Gly Ile Ser Gly Met Ala Leu			
225	230	235	
agt ccc atg act aac aat ctc tat tac agt cct gta gct tcc acc agt 768			
Ser Pro Met Thr Asn Asn Leu Tyr Tyr Ser Pro Val Ala Ser Thr Ser			
240	245	250	255
ttg tat tat gtt aac acg gaa caa ttc aga aca tcc gat tat caa cag 816			
Leu Tyr Tyr Val Asn Thr Glu Gln Phe Arg Thr Ser Asp Tyr Gln Gln			
260	265	270	
aat gac ata cat tac gaa gga gtc caa aat att ttg gat acc caa tcg 864			
Asn Asp Ile His Tyr Glu Gly Val Gln Asn Ile Leu Asp Thr Gln Ser			
275	280	285	
tcc gct aaa gta gta tca aag agt ggc gtt ctc ttc ttc gga ttg gtg 912			
Ser Ala Lys Val Val Ser Lys Ser Gly Val Leu Phe Phe Gly Leu Val			
290	295	300	
ggc gat tca gct ctt ggc tgc tgg aac gaa cat cga aca ctt gaa aga 960			
Gly Asp Ser Ala Leu Gly Cys Trp Asn Glu His Arg Thr Leu Glu Arg			
305	310	315	
cac aat atc cgt acc gtc gct caa agt gat gag act ctt caa atg atc 1008			
His Asn Ile Arg Thr Val Ala Gln Ser Asp Glu Thr Leu Gln Met Ile			
320	325	330	335
gct agc atg aag att aag gaa gct ctt cca cac gtg cct ata ttc gat 1056			
Ala Ser Met Lys Ile Lys Glu Ala Leu Pro His Val Pro Ile Phe Asp			
340	345	350	
agg tat ata aac cgt gaa tac ata ttg gtt tta agt aac aaa atg caa 1104			
Arg Tyr Ile Asn Arg Glu Tyr Ile Leu Val Leu Ser Asn Lys Met Gln			

355	360	365
aaa atg gtg aat aat gac ttc aac ttc gac gat gtt aac ttc aga att 1152		
Lys Met Val Asn Asn Asp Phe Asn Phe Asp Asp Val Asn Phe Arg Ile		
370	375	380

atg aac gcg aat gta aac gaa ttg ata ttg aac act cgt tgc gaa aat 1200
Met Asn Ala Asn Val Asn Glu Leu Ile Leu Asn Thr Arg Cys Glu Asn
385 390 395

ccc gat aat gat cga aca cct ttc aaa att tca atc cat ttg taa 1245
Pro Asp Asn Asp Arg Thr Pro Phe Lys Ile Ser Ile His Leu
400 405 410

<210> 7
 <211> 1830
 <212> DNA
 <213> Apis mellifera
 <220>
 <221> CDS
 <222> (35).. (1669)
 <220>
 <221> sig_peptide
 <222> (35).. (94)
 <220>
 <221> mat_peptide
 <222> (95).. (1666)
 <400> 7

gtcaattgga aaatatctgt attatcctag aaaa atg aca aag tgg ttg ttg ctg 55
Met Thr Lys Trp Leu Leu Leu
-20 -15

gtg gtg tgc ctt ggt ata gct tgt caa gat gta aca agc gca gct gtg 103
Val Val Cys Leu Gly Ile Ala Cys Gln Asp Val Thr Ser Ala Ala Val
-10 -5 1

aat cat caa aga aaa tct gca aat aat ttg gca cat tct atg aaa gtg 151
 Asn His Gln Arg Lys Ser Ala Asn Asn Leu Ala His Ser Met Lys Val

5

10

15

atc tac gaa tgg aaa cac att gat ttt gat ttc ggt agc gat gaa aga 199
 Ile Tyr Glu Trp Lys His Ile Asp Phe Asp Phe Gly Ser Asp Glu Arg

20

25

30

35

aga gat gct gcg att aaa tct ggc gaa ttt gat cac aca aaa aat tat 247
 Arg Asp Ala Ala Ile Lys Ser Gly Glu Phe Asp His Thr Lys Asn Tyr

40

45

50

cct ttc gat gtg gac aga tgg cgt gat aag aca ttt gtc acc ata gaa 295
 Pro Phe Asp Val Asp Arg Trp Arg Asp Lys Thr Phe Val Thr Ile Glu

55

60

65

agg aac aat ggt gta cct tct tct ttg aac gtg gta act aat aaa aag 343
 Arg Asn Asn Gly Val Pro Ser Ser Leu Asn Val Val Thr Asn Lys Lys

70

75

80

ggc aaa ggt gga cct ctt cta cga cca tat cct gat tgg tog ttt gcc 391
 Gly Lys Gly Gly Pro Leu Leu Arg Pro Tyr Pro Asp Trp Ser Phe Ala

85

90

95

aaa tac gaa gat tgc tct gga att gtg agc gct ttc aaa att gcg gtc 439
 Lys Tyr Glu Asp Cys Ser Gly Ile Val Ser Ala Phe Lys Ile Ala Val

100

105

110

115

gac aaa ttt gac aga tta tgg gtt ctg gac tca ggt ctt gtc aat aat 487
 Asp Lys Phe Asp Arg Leu Trp Val Leu Asp Ser Gly Leu Val Asn Asn

120

125

130

aat caa cct atg tgc tct cca aaa ttg tta acc ttt gat ctg aaa acc 535
 Asn Gln Pro Met Cys Ser Pro Lys Leu Leu Thr Phe Asp Leu Lys Thr

135

140

145

tca aaa ttg gtt aag caa gtc gag ata cca cat aat att gcc gta aac 583
 Ser Lys Leu Val Lys Gln Val Glu Ile Pro His Asn Ile Ala Val Asn

150

155

160

gcc acc aca gga atg gga gaa tta gtt tca cta gct gtt caa gct ata 631
 Ala Thr Thr Gly Met Gly Glu Leu Val Ser Leu Ala Val Gln Ala Ile

165

170

175

gat cgt acg aat act atg gtg tac ata gca gac gaa aaa ggc gaa ggt 679
 Asp Arg Thr Asn Thr Met Val Tyr Ile Ala Asp Glu Lys Gly Glu Gly

180

185

190

195

tta atc atg tat caa aac tcc gac gat tcc ttc cat cga ttg act tcc 727
 Leu Ile Met Tyr Gln Asn Ser Asp Asp Ser Phe His Arg Leu Thr Ser

200

205

210

aat act ttc gat tac gat ccc aga tat acc aaa ttg aca gtc gct gga 775
 Asn Thr Phe Asp Tyr Asp Pro Arg Tyr Thr Lys Leu Thr Val Ala Gly

215

220

225

gaa agt ttc aca gtg aaa aat gga att tat gga att gca ctt agt ccc 823
 Glu Ser Phe Thr Val Lys Asn Gly Ile Tyr Gly Ile Ala Leu Ser Pro

230

235

240

gtg acg aac aat ctt tat tac agc cct ctt ctt tct cac ggt ttg tat 871
 Val Thr Asn Asn Leu Tyr Tyr Ser Pro Leu Leu Ser His Gly Leu Tyr

245

250

255

tat gtt gat acg gaa caa ttc agc aat cca caa tat gaa gaa aat aac 919
 Tyr Val Asp Thr Glu Gln Phe Ser Asn Pro Gln Tyr Glu Glu Asn Asn

260

265

270

275

gtg caa tat gaa gga tct caa gat att ttg aac act caa tca ttc ggt 967
 Val Gln Tyr Glu Gly Ser Gln Asp Ile Leu Asn Thr Gln Ser Phe Gly

280

285

290

aaa gta gta tcg aaa aat ggc gtc ctt ttc ttg gga ctc gtg ggt aat 1015
 Lys Val Val Ser Lys Asn Gly Val Leu Phe Leu Gly Leu Val Gly Asn
 295 300 305

tca ggt att gcc tgc gtg aat gaa cat caa gta ctt cag aga gaa agt 1063
 Ser Gly Ile Ala Cys Val Asn Glu His Gln Val Leu Gln Arg Glu Ser
 310 315 320

ttt gat gtt gtc gct cag aat gaa gag aca ctt caa atg atc gtt agt 1111
 Phe Asp Val Val Ala Gln Asn Glu Glu Thr Leu Gln Met Ile Val Ser
 325 330 335

atg aaa atc atg gaa aat ctt cca caa tcc ggc aga att aat gat cct 1159
 Met Lys Ile Met Glu Asn Leu Pro Gln Ser Gly Arg Ile Asn Asp Pro
 340 345 350 355

gaa ggc aat gaa tat atg ttg gct ttg agt aac aga atg caa aaa ata 1207
 Glu Gly Asn Glu Tyr Met Leu Ala Leu Ser Asn Arg Met Gln Lys Ile
 360 365 370

ata aac aat gat ttt aat ttc aac gac gta aat ttc cga att ttg ggt 1255
 Ile Asn Asn Asp Phe Asn Phe Asn Asp Val Asn Phe Arg Ile Leu Gly
 375 380 385

gcg aat gta gat gac tta atg aga aac act cgt tgc gga aga tat cac 1303
 Ala Asn Val Asp Asp Leu Met Arg Asn Thr Arg Cys Gly Arg Tyr His
 390 395 400

aat cag aat gct ggc aat cag aat gct gac aat cag aat gct gac aat 1351
 Asn Gln Asn Ala Gly Asn Gln Asn Ala Asp Asn Gln Asn Ala Asp Asn
 405 410 415

cag aat gct aac aat cag aat gct gat aat cag aat gct aac aaa caa 1399
 Gln Asn Ala Asn Asn Gln Asn Ala Asp Asn Gln Asn Ala Asn Lys Gln
 420 425 430 435

aat ggt aat aga caa aat gat aac aga cag aat gat aac aag caa aat 1447
 Asn Gly Asn Arg Gln Asn Asp Asn Arg Gln Asn Asp Asn Lys Gln Asn

440

445

450

ggt aac aga cag aat gat aac aag caa aat ggt aac aga cag aat gat 1495
 Gly Asn Arg Gln Asn Asp Asn Lys Gln Asn Gly Asn Arg Gln Asn Asp

455

460

465

aac aag caa aat ggt aac aga caa aat ggt aac aaa cag aat gat aac 1543
 Asn Lys Gln Asn Gly Asn Arg Gln Asn Gly Asn Lys Gln Asn Asp Asn

470

475

480

aag caa aat ggt aac aga cag aat gat aac aag agg aat ggt aac agg 1591
 Lys Gln Asn Gly Asn Arg Gln Asn Asp Asn Lys Arg Asn Gly Asn Arg

485

490

495

caa aat gat aat caa aat aat cag aat gat aat aat cga aat gat aat 1639
 Gln Asn Asp Asn Gln Asn Asn Gln Asn Asp Asn Asn Arg Asn Asp Asn

500

505

510

515

caa gtt cat cat tct tca aaa tta cat taa atcaatcaat tatcaattaa aat 1692
 Gln Val His His Ser Ser Lys Leu His

520

caattaatta agatgtaaat caaattatit tttaaaatat ttttcgatg taaacaaaat 1752
 tttgtaaaat ctttcattat attataaata aataaaataa atatcgtttt cgcataaaaa 1812
 aaaaaaaaaa aaaaaaaaaa 1830

<210> 8

<211> 1430

<212> DNA

<213> Apis mellifera

<220>

<221> CDS

<222> (46).. (1341)

<220>

<221> sig_peptide

<222> (46).. (102)

<220>

<221> mat_peptide

<222> (103).. (1341)

<220>

<221> UNSURE

<222> (1134)

<223> n=a or g or c or t

<400> 8

ttcacgtaca atattccatt gcttcgttac togcagctta gaaaa atg aca aga ttg 57

Met Thr Arg Leu

-19

ttt atg ctg gta tgc ctt ggc ata gtt tgt caa ggt acg aca ggc aac 105

Phe Met Leu Val Cys Leu Gly Ile Val Cys Gln Gly Thr Thr Gly Asn

-15

-10

-5

1

att ctt cga gga gag tct tta aac aaa tca tta ccc atc ctt cac gaa 153

Ile Leu Arg Gly Glu Ser Leu Asn Lys Ser Leu Pro Ile Leu His Glu

5

10

15

tgg aaa ttc ttt gat tat gat ttc ggt agc gat gaa aga aga caa gat 201

Trp Lys Phe Phe Asp Tyr Asp Phe Gly Ser Asp Glu Arg Arg Gln Asp

20

25

30

gca att cta tct ggc gaa tac gac tac aag aat aat tat cca tcc gac 249

Ala Ile Leu Ser Gly Glu Tyr Asp Tyr Lys Asn Asn Tyr Pro Ser Asp

35

40

45

att gac caa tgg cat gat aag att ttt gtc acc atg ctg aga tac aat 297

Ile Asp Gln Trp His Asp Lys Ile Phe Val Thr Met Leu Arg Tyr Asn

50

55

60

65

ggc gta cct tcc tct ttg aac gtg ata tct aaa aag gtc ggt gat ggt 345

Gly Val Pro Ser Ser Leu Asn Val Ile Ser Lys Lys Val Gly Asp Gly

70	75	80
ggt cct ctt cta caa cct tat ccc gat tgg tcg ttt gct aaa tat gac 393		
Gly Pro Leu Leu Gln Pro Tyr Pro Asp Trp Ser Phe Ala Lys Tyr Asp		
85	90	95
gat tgc tct gga atc gtg agc gcc tca aaa ctt gcg atc gac aaa tgc 441		
Asp Cys Ser Gly Ile Val Ser Ala Ser Lys Leu Ala Ile Asp Lys Cys		
100	105	110
gac aga ttg tgg gtt ctg gac tca ggt ctt gtc aat aat act caa ccc 489		
Asp Arg Leu Trp Val Leu Asp Ser Gly Leu Val Asn Asn Thr Gln Pro		
115	120	125
atg tgt tct cca aaa ctg ctc acc ttt gat ctg act acc tcg caa ttg 537		
Met Cys Ser Pro Lys Leu Leu Thr Phe Asp Leu Thr Thr Ser Gln Leu		
130	135	140
ctc aag caa gtt gaa ata cca cat gat gtt gcc gta aat gcc act aca 585		
Leu Lys Gln Val Glu Ile Pro His Asp Val Ala Val Asn Ala Thr Thr		
150	155	160
gga aag gga aga tta tca tct cta gct gtt caa tct tta gat tgc aat 633		
Gly Lys Gly Arg Leu Ser Ser Leu Ala Val Gln Ser Leu Asp Cys Asn		
165	170	175
aca aat agc gat act atg gtg tac ata gca gac gag aaa ggt gaa ggt 681		
Thr Asn Ser Asp Thr Met Val Tyr Ile Ala Asp Glu Lys Gly Glu Gly		
180	185	190
tta atc gtg tat cat aat tct gat gat tcc ttc cat cga ttg act tcc 729		
Leu Ile Val Tyr His Asn Ser Asp Asp Ser Phe His Arg Leu Thr Ser		
195	200	205
aac act ttc gat tac gat cct aaa ttt acc aaa atg acg atc gat gga 777		
Asn Thr Phe Asp Tyr Asp Pro Lys Phe Thr Lys Met Thr Ile Asp Gly		

210	215	220	225
gaa agt tac aca gcc caa gat gga att tct gga atg gct ctt agt ccc 825			
Glu Ser Tyr Thr Ala Gln Asp Gly Ile Ser Gly Met Ala Leu Ser Pro			
	230	235	240
atg act aac aat ctc tat tac agt cct gta gct tcc acc agt ttg tat 873			
Met Thr Asn Asn Leu Tyr Tyr Ser Pro Val Ala Ser Thr Ser Leu Tyr			
	245	250	255
tat gtt aac acg gaa caa ttc aga aca tcc gat tat caa cag aat gac 921			
Tyr Val Asn Thr Glu Gln Phe Arg Thr Ser Asp Tyr Gln Gln Asn Asp			
	260	265	270
ata cat tac gaa gga gtc caa aat att ttg gat acc caa tcg tcc gct 969			
Ile His Tyr Glu Gly Val Gln Asn Ile Leu Asp Thr Gln Ser Ser Ala			
	275	280	285
aaa gta gta tca aag agt ggc gtt ctc ttc ttc gga ttg gtg ggc gat 1017			
Lys Val Val Ser Lys Ser Gly Val Leu Phe Phe Gly Leu Val Gly Asp			
290	295	300	305
tca gct ctt ggc tgc tgg aac gaa cat cga aca ctt gaa aga cac aat 1065			
Ser Ala Leu Gly Cys Trp Asn Glu His Arg Thr Leu Glu Arg His Asn			
	310	315	320
atc cgt acc gtc gct caa agt gat gag act ctt caa atg atc gct agc 1113			
Ile Arg Thr Val Ala Gln Ser Asp Glu Thr Leu Gln Met Ile Ala Ser			
	325	330	335
atg aag att aag gaa gct ctn cca cac gtg cct ata ttc gat agg tat 1161			
Met Lys Ile Lys Glu Ala Leu Pro His Val Pro Ile Phe Asp Arg Tyr			
	340	345	350
ata aac cgt gaa tac ata ttg gtt tta agt aac aaa atg caa aaa atg 1209			
Ile Asn Arg Glu Tyr Ile Leu Val Leu Ser Asn Lys Met Gln Lys Met			

355	360	365	
gtg aat aat gac ttc aac ttc gac gat gtt aac ttc aga att atg aac 1257			
Val Asn Asn Asp Phe Asn Phe Asp Asp Val Asn Phe Arg Ile Met Asn			
370	375	380	385
gcg aat gta aac gaa ttg ata ttg aac act cgt tgc gaa aat ccc gat 1305			
Ala Asn Val Asn Glu Leu Ile Leu Asn Thr Arg Cys Glu Asn Pro Asp			
	390	395	400
aat gat cga aca cct ttc aaa att tca atc cat ttg taa aatctgagtt tt 1356			
Asn Asp Arg Thr Pro Phe Lys Ile Ser Ile His Leu			
	405	410	
ttgttatata ttaaataattt ctcgaaattt ctttccatta tgaatgtata aaataaatat 1416			
tgttttcgca taat 1430			

<210> 9
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide as PCR sense primer
 <400> 9
 cctagaaaaa tgacaaagtg gttg 24

<210> 10
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide as PCR anti-sense primer
 <400> 10
 gattttacaa aattttgttt acatcg 26

<210> 11

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide as PCR sense primer

<400> 11

gctacatatg aacattcttc gaggagag 28

<210> 12

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide as PCR anti-sense primer

<400> 12

gctaggatcc ctattacaaa tggattgaaa ttttg 35